

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2002, 06:38:56 ; Search time 1709.21 Seconds

(without alignments)  
2605.879 Million cell updates/sec

Title: US-09-622-613A-14

Perfect score: 330  
Sequence: 1 cagaactggcacttcca.....ctggtatcggtcgtgcccg 330

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estln:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hnc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hnc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	40	12.1	500	9	AU087262 AU087262
C 2	39.2	11.9	565	9	AA481151 aa34f11.s
C 3	39.2	11.9	1014	10	B1948321 HVSME1000
C 4	38.2	11.6	1067	12	CNS00C08
C 5	38	11.5	914	12	AZ205202
C 6	37.8	11.5	590	10	AZ205202
C 7	37.6	11.4	655	10	B1814232
C 8	37	11.2	530	12	BG590791
C 9	36.8	11.2	514	9	AV441651
C 10	36.8	11.2	558	12	AZ729728
C 11	36.8	11.2	709	12	AZ729405
C 12	36.4	11.0	428	12	AZ161580
C 13	36.4	11.0	644	12	AQ365154
C 14	36.4	11.0	739	12	AZ196614
C 15	36.2	11.0	561	12	AZ841683
C 16	36.2	11.0	652	12	AM690825
C 17	36	10.9	853	12	CNS023KH

C 18	36	10.9	918	12	CNS03XDD
C 19	35.8	10.8	425	12	A1176919
C 20	35.8	10.8	544	9	AM299150
C 21	35.8	10.8	604	9	BE204104
C 22	35.8	10.8	628	9	BE204201
C 23	35.8	10.8	644	9	BE202886
C 24	35.8	10.8	720	9	BE202887
C 25	35.8	10.8	1025	12	A2547484
C 26	35.6	10.8	407	9	AU087119
C 27	35.6	10.8	465	12	BH169613
C 28	35.6	10.8	506	9	A1117048
C 29	35.6	10.8	528	9	A1119176
C 30	35.6	10.8	541	12	CNS04KUS
C 31	35.6	10.8	720	10	B1683811
C 32	35.4	10.7	500	9	AM200850
C 33	35.4	10.7	644	12	AZ725604
C 34	35.2	10.7	340	10	U92731
C 35	35	10.6	507	12	A2930800
C 36	35	10.6	640	12	AZ210822
C 37	35	10.6	1101	12	CNS00GY6
C 38	34.8	10.5	364	10	BE288646
C 39	34.8	10.5	471	12	AQ638092
C 40	34.8	10.5	495	9	AL388920
C 41	34.8	10.5	548	12	AQ885225
C 42	34.8	10.5	560	9	AM685365
C 43	34.8	10.5	580	9	A1533845
C 44	34.8	10.5	611	9	BE123874
C 45	34.8	10.5	621	10	B1640493

#### ALIGNMENTS

RESULT 1  
LOCUS AU087262/c 500 bp mRNA linear EST 27-JAN-2001  
DEFINITION AU087262 Sugano Malaria cDNA library Plasmodium falciparum cDNA  
ACCESSION AU087262  
VERSION AU087262.1 GI:12389403  
KEYWORDS EST.  
SOURCE malaria parasite P. falciparum.  
ORGANISM Plasmodium falciparum  
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
REFERENCE 1 (bases 1 to 500)  
Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.  
FULL-LENGTH a database for a full-length enriched cDNA library  
from human malaria parasite, Plasmodium falciparum  
Nucleic Acids Res. 29 (1), 70-71 (2001)  
20574754  
COMMENT Contact: Junichi Watanabe  
Institute of Medical Science  
The University of Tokyo, Department of Parasitology  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Tel: 81-3-5449-5378  
Fax: 81-3-5449-5410  
Email: jwatanab@med.s.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Suyama, A. and Sugano  
S. Construction and characterization of a full length-enriched  
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).

#### FEATURES

source  
1..500  
/organism="Plasmodium falciparum"  
/strain="3D7"  
/db\_xref="taxon:5833"  
/clone="XpP4095"  
/clone\_lib="Sugano Malaria cDNA library"  
/dev\_stage="erythrocytic stage"  
BASE COUNT 256 a 41 c 55 g 148 t  
ORIGIN

Query Match 12.1%; Score 40; DB 9; Length 500;





	source	1..914 /organism="Strongyloides colonicus purpuratus" /db_xref="taxon:7668" /clone_plate=100 Col-24 Row=M" /clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library" /note="Organ: sperm; Vector: BACs3.6; BAC clones in E-Colli DH10B"
BASE COUNT	210 a 208 c 107 g 387 t	2 others
ORIGIN		
Query Match	11.5%; Score 38; DB 12; Length 914;	
Best Local Similarity	52.5%; Pred. No. 5.7;	
Matches	83; Conservative 0; Mismatches 75; Indels 0; Gaps 0;	
OY	108 taacattcaccatctcttcgtctactactgcttaaacgtatctgcagtggttataca 167	
Dd	285 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 344	
OY	168 catgaacctctgtctactactcggttccagctgaacactgcagctgctactcatac 227	
Dd	345 TATTCTGTTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 404	
OY	228 tcggcgctgcggccgctactctcttcgtctactgaaacta 265	
Dd	405 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 442	
RESULT 6	BIR14232	590 bp mRNA linear EST 03-OCT--2001
BIR14232/c	PfStoRaallh12.y2 plasmodium falci parum 3D7 aseual cDNA Plasmidium	
LOCUS	falciparum cDNA 5' similar to TR:O7J336 O7J336 PfC0425W PROTEIN. ;	
DEFINITION	mRNA sequence.	
ACCESSION	BIR14232	
VERSION	BIR14232.1 GI:15906641	
KEYWORDS	EST.	
SOURCE	malaria parasite P. falciparum.	
ORGANISM	Plasmodium falciparum	
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	
AUTHORS	Tang,R., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Page,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowen,Y., Gibbons,M., Ritzer,E., Bennett,J., Jentes,E., Ronko,I., Tsagaris,N.,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Waterston,R., Wilson,R. and Sibley,D. Mashu Plasmodium EST Project Unpublished (2001) Contact: L. David Sibley Washu Plasmodium EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: eslewatson.wustl.edu Library was constructed by Debopam Chakrabarti DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: L. David Sibley (lsibley@orcm.wustl.edu), Washington University Seq primer: -40UP from Glpco High quality sequence stop: 428. Location/Qualifiers 1..590 /organism="Plasmodium falciparum" /db_xref="taxon:5833" /clone_lib="Plasmodium falciparum 3D7 aseual cDNA" /lab_host="DH10B (Genethog, Invitrogen, Inc.)" /note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2: XhoI. Library was constructed by Debopam Chakrabarti. Total RNA samples were isolated from mixed stage saponin(0.1%)ysed P. falciparum 3D7 infected	
TITLE	JOURNAL	
COMMENT		
FEATURES	source	

Query Match	11.5%	Score 37.8	DB 10	Length 590
Best Local Similarity	49.7%	Pred. No. 5.3		
Matches 96	Conservative 0	Mismatches 97	Indels 0	Gaps 0
OY	32	tcatacaactccgcatctcgcgaactatcatgacaacaacatctacatcgctgtg	91	
Db	367	TTATCATCATCGTTATCATCATCGTTATCATCATCGTTATCATCATCGTTATTT	308	
OY	92	gtcagtcgaacacgctgttaacactcttcacatcctctcgcctactactcgttaagatctc	151	
Db	307	ACATCATCATCTATATATCATCATCATCATCGTTATTTATCATCATCATCT	248	
OY	152	gcactggtctatacaacatgacgctcgtctactactcgtttccagtcgacacttgca	211	
Db	247	ATATCTACCTTTTACACAGTGCATCGCTTCTTACTCTCTTATGGTTATATCATTTATA	188	
OY	212	ctcgcactactctat	224	
Db	187	CTGTTGTTCATAT	175	

erythrocytes by the acidic guanidinium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tricet mRNA isolation system (Promega, WI) using streptavidin Magnosphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap cDNA synthesis kit (Stratagene, CA). The average size of the cDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precipitated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."

BASE COUNT 285 a 63 c 95 g 147 t

ORIGIN

1. .655  
/organism="Solanum tuberosum"  
/cultivar="kennebec"  
/db\_xref="taxon:4113"  
/clone="BPL16E4"  
/clone\_1id="P. infestans-challenged leaf"  
/tissue\_type="leaf"  
/dev\_stage="6 week old"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:

RESULT 7  
BG590791/c  
LOCUS  
DEFINITION  
ES7498633 P. infestans-challenged leaf Solanum tuberosum cDNA clone  
BPL16E4 5' sequence, mRNA sequence.  
ACCESSION  
BG590791  
VERSION  
BG590791.1 GI:13608931  
KEYWORDS  
EST.  
SOURCE  
Solanum tuberosum  
ORGANISM  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
REFERENCE  
1 (bases 1 to 655)  
Zhang, P., Hernandez, M., Tornqvist, C.-E., Wirtz, U., Loukolanov, A.,  
Rangel, P., Heberleach, G.T., Cho, J., Chilingiro, A., Bougri, O., Bueli,  
C.R., Ronning, C.M., Helgeson, J. and Baker, B.  
Generation of ESTs from Potato Leaves Challenged with Phytophthora  
infestans, Incompatible Reaction  
Unpublished (2000)  
JOURNAL  
COMMENT  
Contact: Cathy Ronning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: M13F-R.  
location/Qualifiers  
1. .655  
/organism="Solanum tuberosum"  
/cultivar="kennebec"  
/db\_xref="taxon:4113"  
/clone="BPL16E4"  
/clone\_1id="P. infestans-challenged leaf"  
/tissue\_type="leaf"  
/dev\_stage="6 week old"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:



DB 459 TTTTCACAAATGATATCATTCGGTATTTTCTTCACTGGTAGAGCTTTCTTGATCAGCTTTTG 400  
 QY 165 caacatgaacgctctctctactactcgtctccagctgaacacttgcaactctactat 224  
 DB 399 ACACCTTAACATATCATGTGTCAGCAACACACTGAGACATCTGACGAGTACTTTCAT 340  
 QY 225 caatccgctcgtgcccgtactctctcgtactgaactaactacatctcggtta 280  
 DB 339 CATTAGCTGACCAACCCCTGACCTGTATCTTGATTTGCAATAGCTCTGCTTCA 284

RESULT 10  
 A2729728 558 bp DNA linear GSS 25-JAN-2001  
 LOCUS RPCI-24-99F3.TV RPCI-24 Mus musculus genomic clone RPCI-24-99F3,  
 DEFINITION DNA sequence.  
 ACCESSION A2729728  
 VERSION A2729728.1 GI:12487775  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 558)  
 Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,  
 Russell,D., de Jong,P. and Fraser,C.M.  
 Mouse BAC End sequences from Library RPCI-24  
 Unpublished (1999)  
 Other\_GSSs: RPCI-24-99F3.TJ  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: [http://www.tigr.org/tldb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 99 row: F column: 3  
 Seq primer: T7  
 Class: BAC ends.

# FEATURES

source Location/Qualifiers  
 1..558  
 /organism="Mus musculus"  
 /strain="C57Bl/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-24-99F3"  
 /clone\_1lb="RPCI-24"  
 /sex="Male"  
 /cell\_type="Spleen/Brain"  
 /note="Vector: pTARBAC1; Site.1: BamHI; Site.2: BamHI; RPCI-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57Bl/6J DNA."  
 BASE COUNT 213 a 90 c 142 g 113 t  
 ORIGIN

Query Match 11.2%; Score 36.8; DB 12; Length 558;  
 Best Local Similarity 49.0%; Pred. No. 9.8;  
 Matches 98; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 74 acctcacatcgtgtgctcagtcgcaaacgcttaaacacttcacatctctctgcta 133  
 DB 544 ACCTAGGCAATGACGTTTACCTCTTCGAGACTTATGCTAATGAAGCTTCCCTTTC 485  
 QY 134 ctactgttaagatattgacatgctggttataacatgaacgcttcgtctactactgct 193

DB 484 TTTCTTTTTCGATATTCGACTGCTGTCACATCGAGGTTTCGGCTCAAACTCTTC 425  
 QY 194 tccagctgaacacttgcaactctctactcactccgctccgctgcccgtactctctc 253  
 DB 424 TCCAGCTGCTGATATTCCTGCTCTCTGCTTGGCCCTCTGTAATTACTCTGCTT 365  
 QY 254 gtactgaactaactacatc 273  
 DB 364 GTCCTCATACTAAGCTGAGC 345

RESULT 11  
 A2729405 709 bp DNA linear GSS 25-JAN-2001  
 LOCUS RPCI-24-99F2.TV RPCI-24 Mus musculus genomic clone RPCI-24-99F2,  
 DEFINITION DNA sequence.  
 ACCESSION A2729405  
 VERSION A2729405.1 GI:12487129  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 709)  
 Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,  
 Russell,D., de Jong,P. and Fraser,C.M.  
 Mouse BAC End sequences from Library RPCI-24  
 Unpublished (1999)  
 Other\_GSSs: RPCI-24-99F2.TJ  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: [http://www.tigr.org/tldb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 99 row: F column: 2  
 Seq primer: T7  
 Class: BAC ends.

# FEATURES

source Location/Qualifiers  
 1..709  
 /organism="Mus musculus"  
 /strain="C57Bl/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-24-99F2"  
 /clone\_1lb="RPCI-24"  
 /sex="Male"  
 /cell\_type="Spleen/Brain"  
 /note="Vector: pTARBAC1; Site.1: BamHI; Site.2: BamHI; RPCI-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57Bl/6J DNA."  
 BASE COUNT 268 a 115 c 176 g 150 t  
 ORIGIN

Query Match 11.2%; Score 36.8; DB 12; Length 709;  
 Best Local Similarity 56.7%; Pred. No. 11;  
 Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 154 actggtgtatcaacatgaacgcttcgtctactactcgtttccagctgaacactgact 213  
 DB 469 ACTGACTGATGTTCAACCTCGAGGAGTTCTGCTCAAACTCTCCAAACGTTGTATTAT 410  
 QY 214 cgtactctatactccggtccggtactctctctcgtactgaactaactaactc 273

Db	A09	CTGCCTTCCTGCTGTGGCCCTCCTTGAAATTAACCTGCTTCCCAACTAAGTAGC	350
RESULT	12		
LOCUS	A2161580/c		
DEFINITION		428 bp DNA linear GSS 29-AUG-2000	
ACCESSION	A2161580		
VERSION	SP_0070.AL_E04.SP6E		
KEYWORDS	Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=70 Col=7 Row=I, DNA sequence.		
SOURCE	A2161580.1 GI:8314253.		
ORGANISM	GSS. Strongylocentrotus purpuratus. Strongylocentrotus purpuratus. Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidae; Euechinoidea; Echinacea; Echinoidae; Strongylocentrotidae; Strongylocentrotus. 1 (bases 1 to 428) Cameron,R.A., Mahalir,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray ,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L. A sea urchin genome project: Sequence scan, virtual map, and additional resources Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)		
REFERENCE			
AUTHORS			
JOURNAL MEDLINE COMMENT			
CONTACT:	Cameron, RA, Davidson, EH, Hood, L		
Division of Biology 156-29			
California Institute of Technology			
Pasadena California 91125, USA			
Tel: (626) 395-8421			
Fax: (626) 793-3047			
Email: acameron@caltech.edu			
Plate: 70 row: I column: 7			
Seq primer: SP6			
Class: BAC ends			
High quality sequence stop: 428.			
FEATURES			
source			
location/Qualifiers			
1..428			
/organism="Strongylocentrotus purpuratus"			
/db_xref="taxon:7668"			
/clone_id="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"			
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli DH10B"			
BASE COUNT	154 a 47 c 78 g 148 t 1 others		
ORIGIN			
Query Match	11.0%; Score 36.4; DB 12; Length 428;		
Best Local Similarity	52.3%; Pred. NO. 11;		
Matches	79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;		
Db	44 cgatcattcgcaacactcatggaacaacatctacatgggttggtgcagtcgaac 103		
OY			
Db	428 CGATCATCATTTATCATTCATCATCATCATCATCATCATCATCGTGTAGTATCATCTTATGA 369		
OY	gtgttaaacaccttccatctctctcttgttactactacgttaaagctatctgcactgtgttta 163		
Db	368 TTATTAAATTTATCATTTATTCATTTACTGTATTACAGATTATTAATCGTNATPAAGTACCATTA 309		
OY			
Db	164 tcaacataaacgtctctgctactactcgttt 194		
OY			
Db	308 TTATTATCATCTCATTCAGTATTTTATCTT 278		
RESULT	13		
LOCUS	A0365154		
DEFINITION	nbbd0063c08r CUCI Rice BAC Library Oryza sativa genomic clone nbbd0063c08r, DNA sequence.		
ACCESSION	A0365154		
LOCUS	A0365154		
DEFINITION	644 bp DNA linear GSS 16-DEC-1999		
ACCESSION	A0365154		

[illegible]

	RESULT	14	
AZ196614	LOCUS	AZ196614	739 bp DNA linear GSS 31-AUG-2000
	DEFINITION	SP_1032_A2_B09-SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone plate=1032 Col=18 Row=C, DNA sequence.	
	ACCESSION	AZ196614	
	VERSION	AZ196614.1	GI:8390437
	KEYWORDS	GSS.	
	SOURCE	Strongylocentrotus purpuratus. Strongylocentrotus purpuratus Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echlinidea; Euechinoidae; Echnacea; Echinoide;	
	ORGANISM	Strongylocentroidae; Strongylocentrotus.	
	REFERENCE	1 (bases 1 to 739) Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L. A sea urchin genome project: Sequence scan, virtual map, and additional resources Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)	
	JOURNAL	Contact: Cameron, RA, Davidson, EH, Hood, L	
	MEDLINE	20402566	
	COMMENT	Cameron, RA, Davidson, EH, Hood, L Division of Biology 156-29 California Institute of Technology Pasadena California 91125, USA Tel.: (626) 395-8421 Fax: (626) 793-3047 Email: acamerone@caltech.edu Plate: 1032 row: C column: 18 Seq primer: SP6 Class: BAC ends High quality sequence stop: 739. Location/Qualifiers  1..739 /organism="Strongylocentrotus purpuratus" /db_xref="taxon:7668" /clone_plate="1032 Col=18 Row=C" /clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library" /note="Organ: sperm; Vector: BAC#3.6; BAC clones in E-Colli DH10B"	
	FEATURES	source	
	BASE COUNT	228 a     131 c     93 g     287 t	
	ORIGIN		
	Query Match	11.0% Score 36.4 DB 12 Length 739;	
	Best Local Similarity	46.5% Pred. No. 14;	
	Matches 100; Conservative	0; Mismatches 106; Indels 0; Gaps 0;	
OY	25 aaacaatcattcaaaacaccgcgaatcatctgtccaacactaatcagtaaacatatcacatc	84	
DB	317 ATATATTATCATCATCATCATCATCATCATCAACAACGTCATTTAGTGCATCATCTATT	376	
OY	85 gttagtcgacgatcgcaaacgggtttaacaaccttcatcatcctcttgtctaactagttaa	144	
DB	377 ATTATTTATTATTATTATGATTAATGTACTTTCTATAATTTGGTTATTATTATTATTA	436	
OY	145 gttacttgacacgggttatataaacgttgaaaggcttgcgttactactcgtttccaagtgaac	204	
DB	437 TATTAATAATTAACCGCATTAATTAACAAATCCAAATTAATTAATTAATTAATTAATTA	496	
OY	205 acttgactgactgactctatcacccc 230		
DB	497 ATTACTCCTATTATTATTAACATTAACCTCC 522		
RESULT	15		
AZ841683	LOCUS	AZ841683	561 bp DNA linear GSS 20-FEB-2001
	DEFINITION	ZMO139N17R Mouse 10kb plasmid U06CLM library Mus musculus genomic clone U06G2M0139N17 R, DNA sequence.	

ACCESSION	AZ841683
VERSION	AZ841683.1
KEYWORDS	GI:13011591
SOURCE	GSS.
ORGANISM	house mouse. Mus musculus
REFERENCE	Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murine: Mus. 1 (bases 1 to 561)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0139 row: N column: 17 Seq primer: CACACAGGAAACACCTATGACC Class: plasmid ends High quality sequence stop: 561.
FEATURES	location/Qualifiers
SOURCE	1. 561 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="U06C2M0139N17" /clone_id="Mouse 10kb plasmid U06C1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb AF129072.1]), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	77 a 138 c 116 g 230 t
ORIGIN	
Query Match	11.0%; Score 36.2; DB 12; Length 561;
Best Local Similarity	56.2%; Pred. No. 14;
Matches 68; Conservative 0; Mismatches 53; Indels 0; Gaps 0;	
0Y	153 caccggtgtatcaacaatgaacggttcgtctacactcctggttccagcgtgaacactgtgac 212
Db	340 CTCGTGTGATTCAATTAACTGTTGCGTCAACCTCCCTCCAAAGCTCAATTCAA 399
0Y	213 tctgaactctatacctccgcgtccgtgcctgactcctctcgtatgaactgaactatcat 272
Db	400 TCTGGCTTGCTCTTCACGCGCTTCTCTTAATTTGTTCTTGCGCTCACTACTAG 459
0Y	273 c 273



Db 460 C 460

Search completed: August 15, 2002, 09:13:06  
Job time: 9250 sec

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